

# Cell cycle prediction

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Updated date: Oct 29, 2020

 An abbreviated version of this protocol was published in eLIFE in Apr 2020

Chromatin accessibility dynamics and single cell RNA-Seq reveal new regulators of regeneration in neural progenitors

DOI: 10.7554/eLife.52648

## Detailed protocol

Cell cycle prediction analysis was performed using the Seurat software in R.

We referenced this vignette to do our analysis:

[https://satijalab.org/seurat/v3.1/cell\\_cycle\\_vignette.html](https://satijalab.org/seurat/v3.1/cell_cycle_vignette.html)

Under the heading: "Assign Cell-cycle Scores"

Reference to the code used to perform analysis and make figures was uploaded to gitlab and has been provided in our paper. The only modification made to the above vignette was removing genes in Seurat's cell cycle modules that we did not have in our dataset and using the remaining genes to run the command "CellCycleScoring":

[https://gitlab.com/akakebee/kakebeen-et-al-2020/-/blob/master/SingleCell\\_1/UMAP/SCRNA\\_Seurat\\_UMAP\\_1.Rmd](https://gitlab.com/akakebee/kakebeen-et-al-2020/-/blob/master/SingleCell_1/UMAP/SCRNA_Seurat_UMAP_1.Rmd)

Under the heading: "## Cell cycle analysis"

**How to cite:** (Readers should cite both the Bio-protocol preprint and the original research article where this protocol was used)

1. Kakebeen, A. and Wills, A. (2020). Cell cycle prediction. Bio-protocol Preprint. [bio-protocol.org/prep585](https://bio-protocol.org/prep585).
2. Kakebeen, A. D., Chitsazan, A. D., Williams, M. C., Saunders, L. M. and Wills, A. E. (2020). Chromatin accessibility dynamics and single cell RNA-Seq reveal new regulators of regeneration in neural progenitors. eLIFE. DOI: [10.7554/eLife.52648](https://doi.org/10.7554/eLife.52648)

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